Inferring Brown-Capped Rosy-Finch demography and breeding distribution trends from long-term wintering data in New Mexico

New Mexico Department of Game and Fish Share with Wildlife Program

Year 2 Second Interim Report

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Brown-capped Rosy-Finch. Photo by Joel Such.

INVESTIGATORS

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ABSTRACT

The three North American Rosy-Finch species (Brown-capped [*Leucosticte australis*], Black [*L. atrata*], and Gray-crowned [*L. tephrocotis*]) are among the most climate-threatened species in the United States. New Mexico is an important location for understanding the effects of climate change because it is the southernmost location in which Brown-capped Rosy-Finches breed and is where all three Rosy-Finch species co-occur during winter. Rosy-Finches are difficult to study during the breeding season due to the high elevation and remoteness of their breeding grounds; therefore, winter studies may lend insight into population trends and provide direction for conservation actions based on knowledge of the breeding origins of wintering birds. Our study investigates long-term demographic and migration trends from wintering Brown-capped Rosy-Finches in New Mexico and to evaluate the efficacy of radio frequency identification (RFID)-equipped artificial feeders to monitor population trends. As of December 2024, analyses of data from RFID feeder visits, mark-recapture activities, and feather samples are underway.

INTRODUCTION

Rosy-Finches are among the most climate-threatened taxa in the United States. Three species are found in North America: Brown-capped (*Leucosticte australis*; BCRF), Black (*L. atrata*; BLRF), and Gray-crowned Rosy-Finches (*L. tephrocotis*; GCRF); hereafter, the three species will be referred to collectively as Rosy-Finches. Rosy-Finches breed exclusively in tundra or alpine tundra ecosystems and because high elevation regions are predicted to be disproportionately impacted by climate change (Pepin et al. 2015), Rosy-Finches face high risk of habitat loss as a result of tree and shrub encroachment (Grace et al. 2002). Furthermore, changes in insect phenology resulting from climate change may negatively impact food availability and quality. All three species of Rosy-Finch are protected by the Migratory Bird Treaty Act, and BCRF and BLRF are listed as Birds of Conservation Concern by the U.S. Fish and Wildlife Service (USFWS 2021). BCRF and BLRF are also included in the Partners in Flight Red Watch list (Rosenberg et al. 2019) and in seven of eight State Wildlife Action Plans throughout their range, including New Mexico. Despite concern for these species, little is known about Rosy-Finch life histories, vital rates, and migration patterns.

Although the three North American Rosy-Finch species have distinct breeding ranges (Fig. 1), they occupy a broader range of habitats and may occur in flocks together outside of the breeding season. During winter Rosy-Finches use a combination of high- and low-elevation areas with varying types and degrees of anthropogenic development, and readily approach artificial feeders. Thus, winter field studies offer a valuable opportunity to efficiently acquire demographic data and biological samples for all three Rosy-Finch species with reduced logistical overhead. Our study leverages an existing long-term (20+ years) mark-recapture dataset with accompanying feather samples from the Sandia Mountains of New Mexico (Fig. 1) and adds a novel component evaluating the efficacy of radio frequency identification (RFID)-equipped artificial feeders to monitor wintering Rosy-Finches. The Sandia Mountains of northern New Mexico is the southernmost wintering locale in which all three Rosy-Finch species co-occur and is the southernmost locale in which any of the three species ever occur (Fig. 1). It is thus a uniquely interesting site at which to study wintering Rosy-Finch populations and document potential impacts of climate change.

We are using this long-term mark-recapture dataset to evaluate trends in Rosy-Finch winter abundance and survival probability. Among Rosy-Finch studies, this mark-recapture dataset is unique in its longevity, sample size, and location at the southern winter range periphery. Studying peripheral species or populations at or near distributional extents is essential for efficient, long-term conservation planning at landscape scales (Steen and Barrett 2015). Peripheral populations can offer insight into a species' physiological tolerances and its capacity to adapt to climate change (e.g., behavior, physiology, dispersal), which is useful for evaluating the effectiveness of potential management actions to curb or offset predicted environmental changes.

To evaluate the migratory connectivity of Rosy-Finch breeding populations to wintering areas in New Mexico, we are conducting hydrogen stable isotope analysis of collected feathers. Hydrogen stable isotope analysis is based on the natural and predictable geographic variation in the ratio of hydrogen isotopes (protium and deuterium) in water molecules, a ratio which is reflected in the tissues of animals based on where the tissues were grown. Rosy-Finches undergo a complete feather molt on the breeding grounds, so analysis of feather tissues collected from birds on their wintering grounds can help identify the breeding areas in which the birds were likely to have bred the previous summer (see Task 3 description for more details). Using stable isotope analysis results, we can investigate the influence of climate covariates at inferred locations of breeding origin or local site conditions that may explain variance in the birds' abundance, survival, or breeding origin.

In addition to analyzing the existing mark-recapture dataset, we initiated a pilot study to evaluate the efficacy of RFID-equipped feeders to improve vital rate estimates and evaluate connectivity among wintering sites. Rosy-Finches are known for nomadic

behavior during winter, in which they may make long-range movements within their winter range for reasons that are not well understood. Such movements (representing temporary emigration) violate the assumptions of many traditional modeling frameworks, meaning that relatively complex frameworks that require robust sample sizes are needed to provide unbiased vital rate estimates. In recent years, multiple avian studies have demonstrated that fitting grain feeders with RFID-enabled "smart" devices is an effective way to acquire visit and movement data from wintering birds marked with tags that the RFID reader can detect at close ranges. This approach was recently used by Latimer and Gardner (2022) for BLRF and GCRF in northern Utah, generating thousands of annual detections to help infer overwinter survival and movement patterns. The RFID component of this study provides a synergistic opportunity to evaluate Rosy-Finch winter movements at small (i.e., within New Mexico) and broad (i.e., across states) scales, given the growing network of RFID-equipped feeders in their wintering range.

Funds from the New Mexico Department of Game and Fish's Share with Wildlife program are being used to support three tasks related to BCRF (below), as part of the larger study focused on all three Rosy-Finch species that is the focus of Whitney Watson's PhD dissertation. As such, we report results for all three species for ease of presentation. The three tasks are as follows:

Task 1: Demographic analysis of mark-recapture data

Task 2: Stable isotope analysis of feather samples

Task 3: Establish new RFID feeders for the winter (2022–2023 field season)

SUMMARY OF REPORTING PERIOD ACTIVITIES

Administration and Project Management

- Whitney successfully completed her fourth semester at New Mexico State University (NMSU) and completed all coursework required for her PhD degree

Task 1

- Whitney continued preliminary survival analyses of mark-recapture data, and has begun analysis in a robust design framework

Task 2

- Whitney received results from 368 BCRF, 114 BLRF, and 136 GCRF feather samples (total 618 feathers) analyzed for stable hydrogen isotope composition by the University of New Mexico Center for Stable Isotopes (UNM CSI)
- An additional 942 feathers (147 BCRF, 504 BLRF, 291 GCRF) have been cleaned and are ready for subsampling and laboratory analysis by UNM CSI

- Whitney has identified a source of known breeding-origin Rosy-Finch feathers, which will increase the precision of assigning breeding origins to the feathers collected during this study after the known-origin feathers are obtained and undergo stable hydrogen isotope analysis
- Undergraduate researcher Kadence Presser continued to work on an independent research project (initiated by Cynthia Dunkleberger) evaluating intra-feather variation in hydrogen isotopic ratios. This work is funded by a separate USDA grant in affiliation with NMSU's Avian Migration Program (https://migration.nmsu.edu/), a mentorship program that aims to prepare students for careers in avian migration conservation

Task 3

- Initiation of the 2024–2025 winter field season, including reinstallation of an RFID-equipped feeder at the Sandia Mountains site (SACR) and Taos Ski Valley (TSV) banding site

Next, we detail progress on project-specific tasks identified in the original scope of work and provide an estimate of percent completion.

Task 1: Demographic analysis of mark-recapture data

We are using existing mark-recapture data and feather samples from a long-term (20+ years) study to evaluate trends in winter abundance and survival probability for all three North American Rosy-Finch species. Whitney has begun analysis of the Rosy-Finch mark-recapture data to estimate Rosy-Finch annual apparent survival. Across the data collection period (2004–2024), the rate of new individuals captured and banded per day of trapping effort varied between 0.3 and 48.1 for BCRF, between 2.0 and 74.1 for BLRF, and between 0.3 and 18.7 for GCRF (Fig. 2). In Bayesian Cormack-Jolly-Seber (CJS) survival analyses including time (winter season), sex, and age as covariates in separate models for each of the three species, the top model for all three species included age class as a covariate, which allowed survival estimates to differ between adults and juveniles and accounted for juveniles becoming adults after their first winter season. See Table 1 for apparent survival probability estimates from these models and Figure 3 for a visualization of the results.

Table 1. Annual apparent survival probability estimates and 95% credible intervals for each of two age classes (juvenile and adult) in each of the three rosy-finch species (brown-capped ["BCRF"], black ["BLRF"], and gray-crowned ["GCRF"]) 2004–2022 from Bayesian Cormack-Jolly-Seber survival analyses. Lower 95% credible interval limits are denoted by "LCL" and upper 95% credible interval limits by "UCL".

	Juveniles			*Adults*		
	Estimate	LCL	UCL	Estimate	LCL	UCL
BCRF	0.43	0.31	0.59	0.38	0.32	0.44
BLRF	0.27	0.20	0.35	0.40	0.34	0.45
GCRF	0.48	0.21	0.87	0.37	0.24	0.50

The CJS survival model is limited in that it only estimates apparent survival, which is a measure of both true survival and site fidelity because mortality cannot be differentiated from emigration. To estimate true survival, we have shifted to an open robust design analysis framework which takes into account secondary sampling occasions to generate more precise survival estimates (Kendall et al. 1997). The open robust design structure considers the population to be closed (no immigration or emigration) between secondary sampling occasions (months within the same winter season) but allows it to be open between primary sampling occasions (winter seasons). As an initial step, we used the robust design framework to model survival for the BLRF, the most data-rich of the three species in this study. In the BLRF analysis, we incorporated time variation as a covariate and found that survival ranged across winter seasons from 0.103 and 0.999 with a mean of 0.444 (Fig. 4). We intend to run analyses in this framework for BCRF and GCRF (i.e., the other two Rosy-Finch species) and to incorporate covariates of age and sex. Eventually, we intend to expand the robust design model to a multistate framework (Kendall et al. 2019), which will allow us to estimate population abundance in addition to survival. We also plan to include additional covariates in these models (in addition to time, age, and sex) including time-varying individual covariates like body condition and time-varying environmental covariates such as precipitation and temperature.

Percent completion: 60%

Task 2: Stable isotope analysis of feather samples

Analysis of hydrogen stable isotopes in feather samples is a widely-used tool to infer an individual bird's breeding origin (location) to evaluate migratory connectivity

patterns. The deuterium (^2H) to protium (^1H) ratio (δ^2H, "delta") in precipitation varies geographically and with elevation (Hobson and Wassenaar 1997, Meehan et al. 2004), and the δ^2H signature of a particular location is reflected in tissues (such as feathers) grown in that location as a result of water and nutrient uptake during tissue formation (Bowen et al. 2005, Wunder 2012). This δ^2H value is traditionally measured in *parts per mille* (i.e., parts per thousand; "‰"), to minimize decimal places in measured ratios of ^2H to ^1H. Because Rosy-Finches undergo complete molts each breeding season (Pyle 1997), a feather collected during the winter is assumed to have been grown on the breeding grounds during the preceding breeding season. We can thus infer breeding locations of individuals by generating probability-of-origin maps (Campbell et al. 2020) based on the δ^2H value of feathers sampled during winter (when Rosy-Finches can be much more readily located and captured) and published δ^2H values of water samples from known locations. Using stable isotope analysis results, we will also investigate the influence of climate covariates at locations of wintering population-level breeding origin or local site conditions that explain variance in abundance or survival (Task 1).

Whitney and our lab technicians have cleaned 1,560 Rosy-Finch feather samples; δ^2H values from 618 of these feathers have been received from UNM CSI to date. The δ^2H values differed significantly among the three species and between juvenile and adults of each individual species (Fig. 5). We did not find significant differences in δ^2H values between sexes in any of the three species (Fig. 6). Over 17 years of feather collection, δ^2H values were significantly positively correlated with winter season in BLRF and GCRF but not in BCRF (Fig. 7). This suggests either a trend toward more southerly and/or lower elevation breeding origins of wintering individuals with time in the two longer-ranging Rosy-Finch species, but trends may alternatively be related to fluctuations in weather conditions on breeding grounds. We then generated probability-of-origin maps for each analyzed feather based on a transfer function developed by Campbell et al. (in press) that correlates feather δ^2H values with average δ^2H values of precipitation in August and September. Our model parameters were based on those of ground foraging, short-distance migrants found by Hobson et al. (2012). Maps for BCRF adult and juvenile individuals suggest breeding origins in the northern, central, and southern regions of the species' range (Fig. 8). Of the individual Rosy-Finches from which feathers were sampled and analyzed, 53 individuals were captured and sampled on multiple occasions (during different winter seasons), and 26 of these individuals were sampled during multiple winter seasons as adults (Fig. 9).

In addition to this work, undergraduate researchers Cynthia and Kadence have worked on an additional study investigating the variation in δ^2H ratios within individual feathers ("intra-feather variation"). These results will determine whether the section of the feather analyzed impacts the resulting δ^2H value for that feather, as has been evidenced in

other studies (e.g., Wassenaar and Hobson 2006, Gordo 2020). To do this, they subdivided 21 BCRF and GCRF feather samples from adults into 5 sections (Fig. 10) and compared δ^2H values across these different sections. We found that sections excluding feather rachis subsampled longitudinally (A1, B1, and C1) did not result in significantly different δ^2H values in BCRF but did vary significantly between A1 and both B1 and C1 in GCRF (Fig. 10b, Fig. 11a). Longitudinal sections containing rachis material (A2 and B2) were significantly different in both BCRF and GCRF (Fig. 11b). In all cases, δ^2H values became increasingly negative as samples were taken from the distal to the proximal end of the feather (Fig. 10a). Lateral comparisons of sections with and without rachis material resulted in significantly different δ^2H values in both species (A1 vs. A2 and B1 vs. B2; Fig. 11c-d). In all cases, δ^2H values of sections containing rachis material were more negative than sections with vane material only. For our breeding origin analysis, subsamples are taken from the distal-most tip of feathers and include rachis material (Fig. 10a). This work suggests that longitudinal location of sampling along the feather as well as the inclusion or exclusion of the rachis may influence a sample's hydrogen stable isotope ratio. This finding will help us standardize duplicate feather samples for the breeding origin study funded by this SwW grant. Undergraduate Kadence presented a poster on this research at the annual American Ornithological Society conference in Estes Park, Colorado in October 2024. She is currently working on performing a similar analysis on BCRF and GCRF juveniles.

During the 2023–2024 winter season, we began collecting multiple feathers from captured Rosy-Finches at SACR to examine inter-feather stable hydrogen isotope variation within individuals. Kadence will analyze these feathers to determine whether the type of feather sampled from an individual bird (e.g., the 1st or 5th rectrix of the tail) affects the resulting isotope value. The feathers collected during the 2023–2024 winter season have been cleaned and will be analyzed by Kadence in spring 2025. Additional collection of multiple feathers from single individuals is ongoing during the 2024–2025 winter season.

Percent completion: 75%

Task 3: Establish new RFID feeders for winter monitoring

RFID reader antenna coils within feeder tray (left) and fully assembled feeder with additional metal layer added atop coils for protection and covered with seed (right).

An RFID reader apparatus consists of Electronic Transponder Analysis Gateway (ETAG) readers powered by 6,400mAh USB battery packs and 3.5 Watt 6 V solar panel arrays (voltaicsystems.com). These readers detect low-frequency (125 kHz) RFID tags affixed to the legs of tagged Rosy-Finches. Birds equipped with RFID tags are detected when they land on or within antenna coils designed to match the tag frequencies. Largely based on trial and error, we utilized numerous iterations of feeder and antenna design to reach an optimal design because antennae were frequently damaged from squirrels chewing on the apparatus and memory card performance was not at desired levels. The final feeder design for 2023–2024 involved "sandwiching" antenna between two sheets of plastic, which minimized the ability of squirrels to access sensitive antennas but still allowed for tag detection. This was a successful strategy, and feeders received minimal squirrel damage over the season. In addition, memory card performance was improved by updating the card housing to include a more robust weatherproof design with less need to move componentry.

During the 2023–2024 winter season, an RFID-equipped feeder was re-deployed at the SACR site from 29 November 2023 to 19 April 2024 and an RFID-equipped feeder was deployed for the first time at the TSV site on 9 January 2024–3 May 2024. Of 53 unique individuals fitted with RFID tags at SACR in the 2023–2024 season, 46 were detected at the RFID feeder. Six tags deployed at SACR in 2022–2023 (all BLRF) were detected by RFID in 2023–2024. At TSV, 23 individuals were RFID tagged in 2023–2024 and 17 of these tags were detected at the RFID feeder later that season. Detections occurred at the highest rates at SACR in the month of February and at 07:00 and 15:00; detections at TSV occurred at the highest rate at 10:00 (Fig.12).

The RFID feeder was redeployed at SACR for the 2024–2025 winter on 1 December 2024. The staff at the TSV site has agreed to let the second RFID feeder be deployed in early January 2025. Data collection will be ongoing throughout the winter. Banding and RFID tagging at SACR occurred on 1, 8, and 17 December 2024; 73 new individuals (61 BLRF, 12 GCRF) were tagged during these sessions. Four BLRF which were first banded during the 2023–2024 season were recaptured this winter. No BCRF have been captured so far this season. Additional banding days at SACR are scheduled for 27 December 2024, 7 January 2025, and every Sunday from mid-January through the end of March 2025.

Percent completion: 75%

PROJECT TIMELINE FOR JANUARY–JUNE 2025

Quarter 1: January 1, 2025 – March 31, 2025:

- Whitney will take her Comprehensive Exam in January 2025 to advance to PhD candidacy
- Whitney will obtain known-origin Rosy-Finch feather samples from collaborators and analyze their stable hydrogen isotopes (using funds from Tracy Aviary Conservation Fund grant) to increase precision of breeding origin assignment of feathers collected on wintering grounds (Task 2)
- Whitney and Kadence will send intra-feather samples from BCRF and GCRF juveniles to UNM lab for analysis (Task 2)
- Whitney and lab technicians will continue to process feather samples to round out samples sizes for each species across years and send to UNM CSI for isotope analysis (Task 2)
- Whitney will continue work on survival and breeding origin analyses (Tasks 1 and 2)
- All project participants will continue 2024–2025 banding season at the SACR and TSV sites and redeploy RFID-equipped feeder at TSV (Tasks 1 and 3)

Quarter 2: April 1, 2025 – June 30, 2025:

- All project participants will finish 2024–2025 banding season at SACR and TSV and remove RFID-equipped feeders from both sites (Tasks 1 and 2)
- Whitney will begin compiling, visualizing, and analyzing RFID data from 2024–2025 winter season (Task 3)
- Whitney, Abby, and Kadence will prepare manuscript detailing intra-feather stable hydrogen isotope study on BCRF and GCRF (Task 2)
- Whitney will complete robust design survival analysis of SACR mark-recapture data up through 2024–2025 season (Task 1)

ACKNOWLEDGEMENTS

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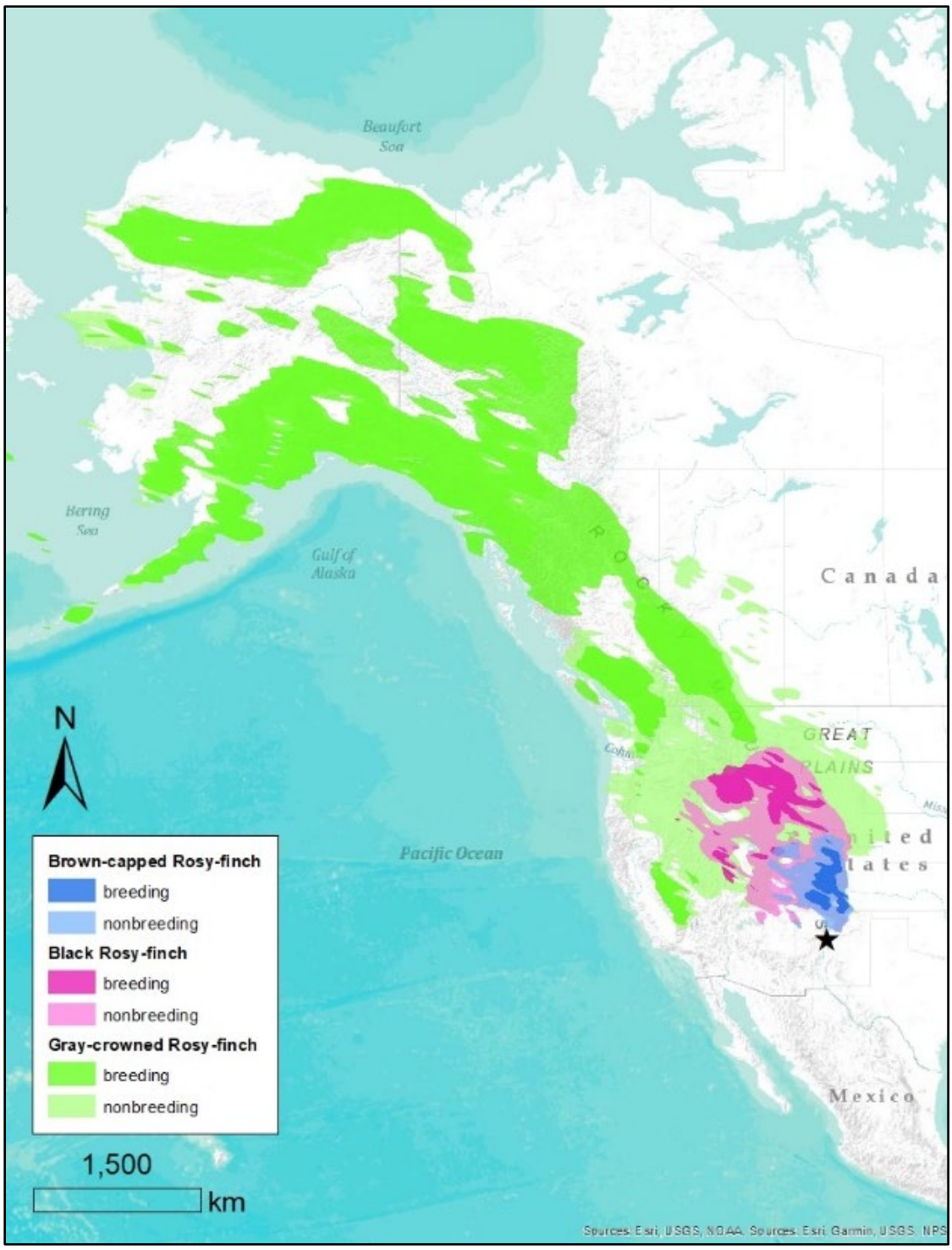

Figure 1. Distributions of each of the three North American Rosy-Finch species. Darker colors represent breeding ranges, and the black star indicates the study site at SACR in northern New Mexico. Distribution data layers from Fink et al. 2022.

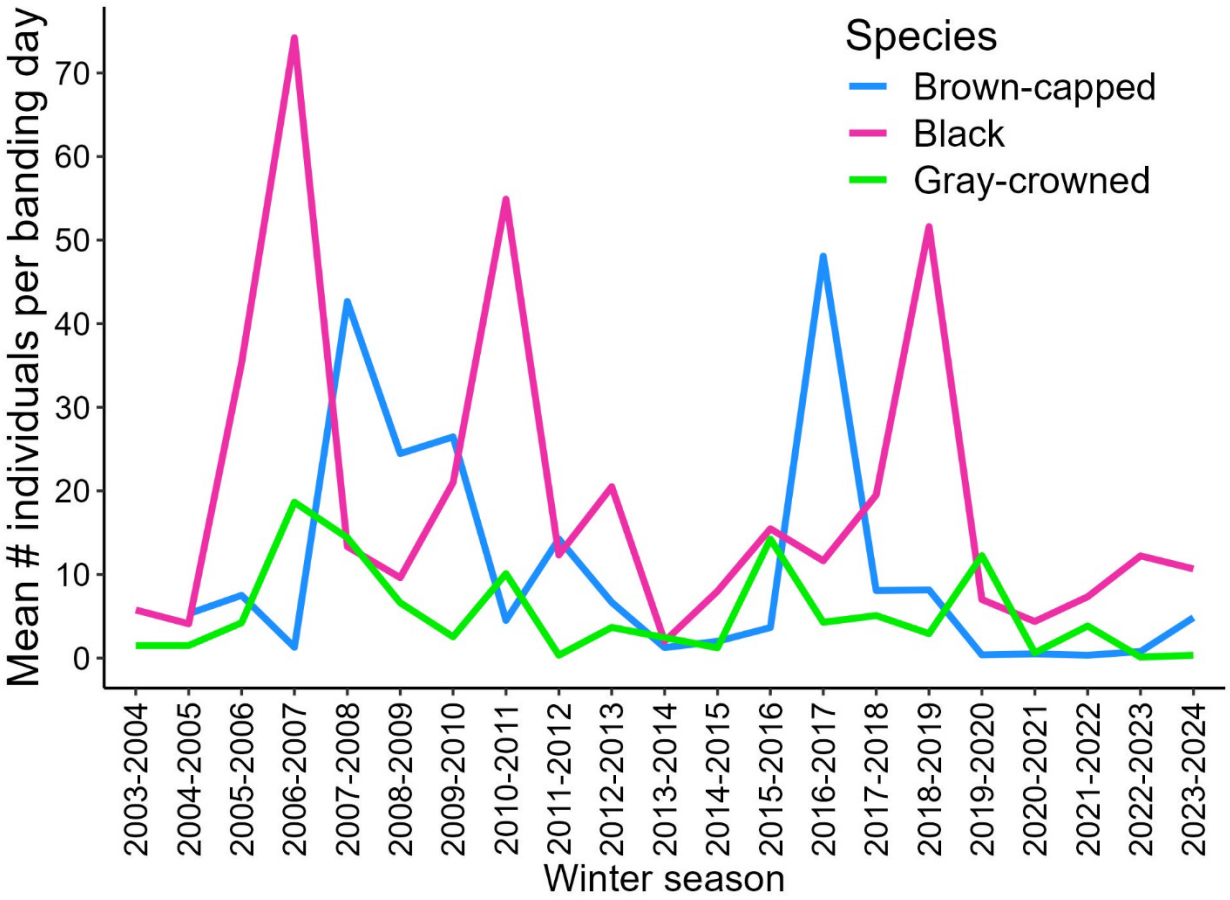

Figure 2. Mean number of unique Rosy-Finches captured by species per successful banding day during each winter banding season at SACR, NM 2003–2024.

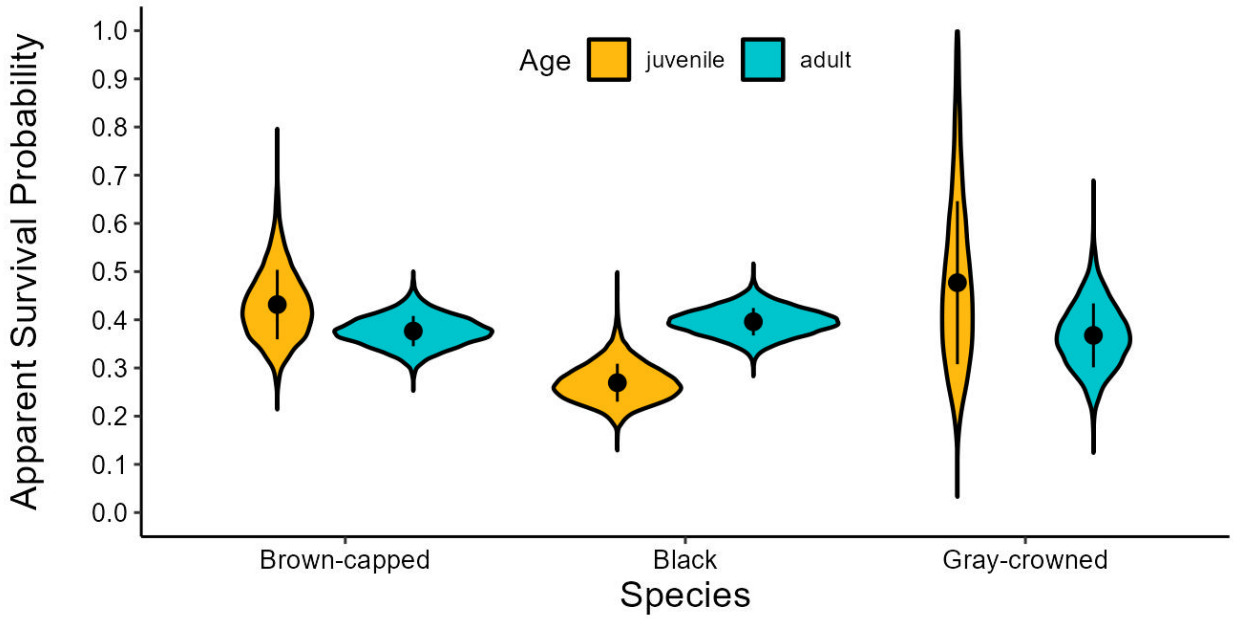

Figure 3. Apparent survival estimates for Rosy-Finches overwintering at SACR from 2004 to 2022 by species and age class. The error bars for each estimate reflect the 95% Bayesian credible interval.

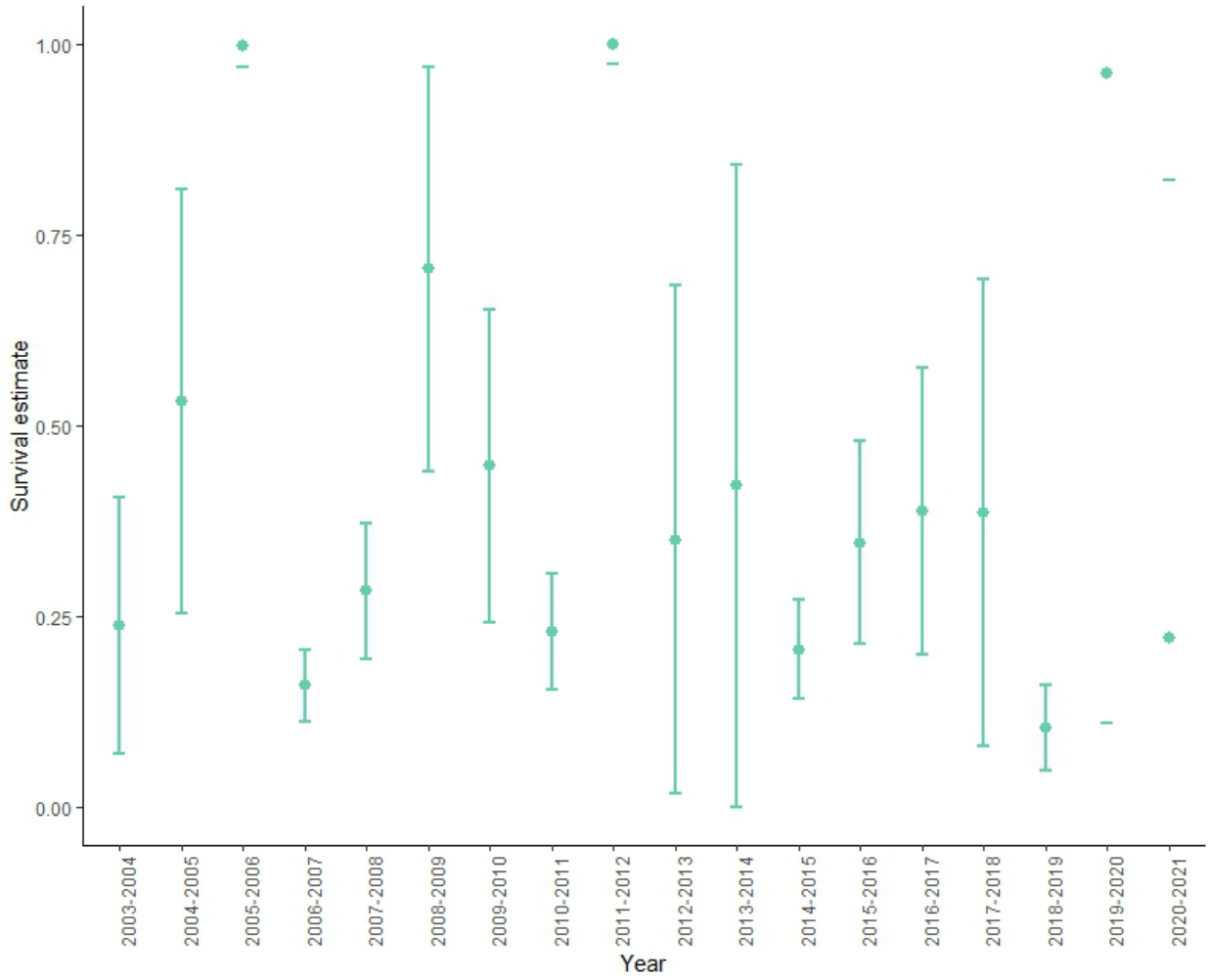

Figure 4. Mean survival estimates (± standard error) of Black Rosy-Finches by year from robust design model with annual variation in survival probability.

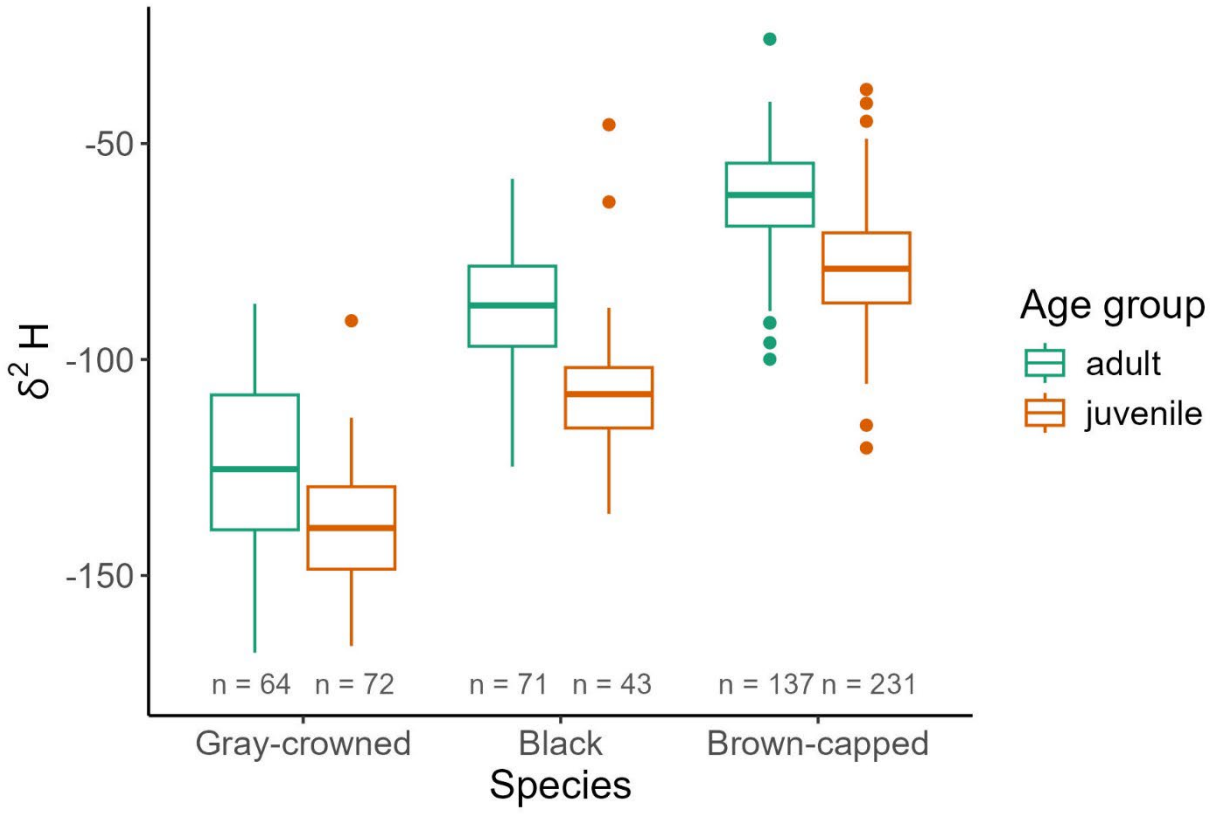

Figure 5. Stable hydrogen isotope values ratio (δ^2H) of Rosy-Finch (*Leucosticte spp.*) feathers sampled at SACR, New Mexico 2004–2022 grouped by species and age group.

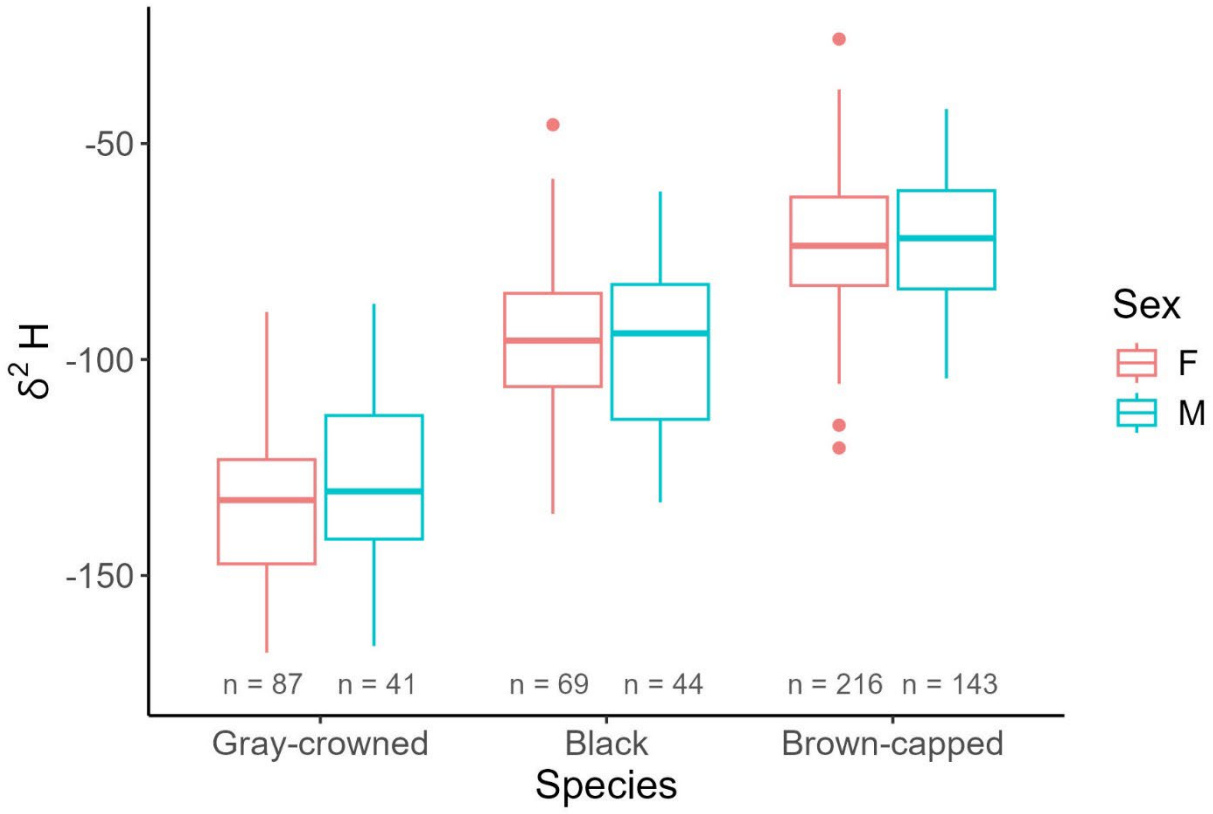

Figure 6. Stable hydrogen isotope values ratio (δ^2H) of Rosy-Finch (*Leucosticte spp.*) feathers sampled at SACR, New Mexico 2004–2022 grouped by species and sex.

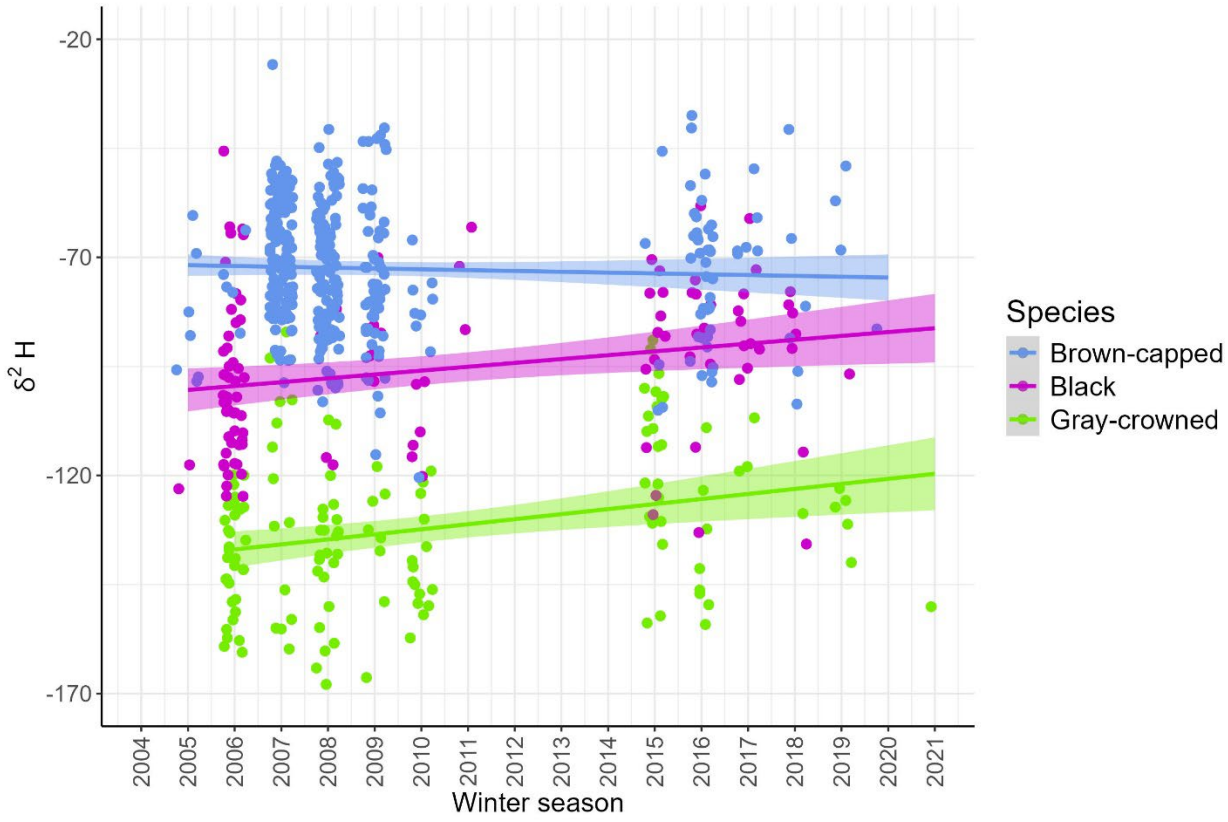

Figure 7. Stable hydrogen isotope ratio values (δ^2H) of individual Rosy-Finch (*Leucosticte spp.*) feathers sampled at SACR, New Mexico 2004–2022 grouped by winter season of sampling. Each point represents one feather. Trend lines show linear trend of δ^2H value with time.

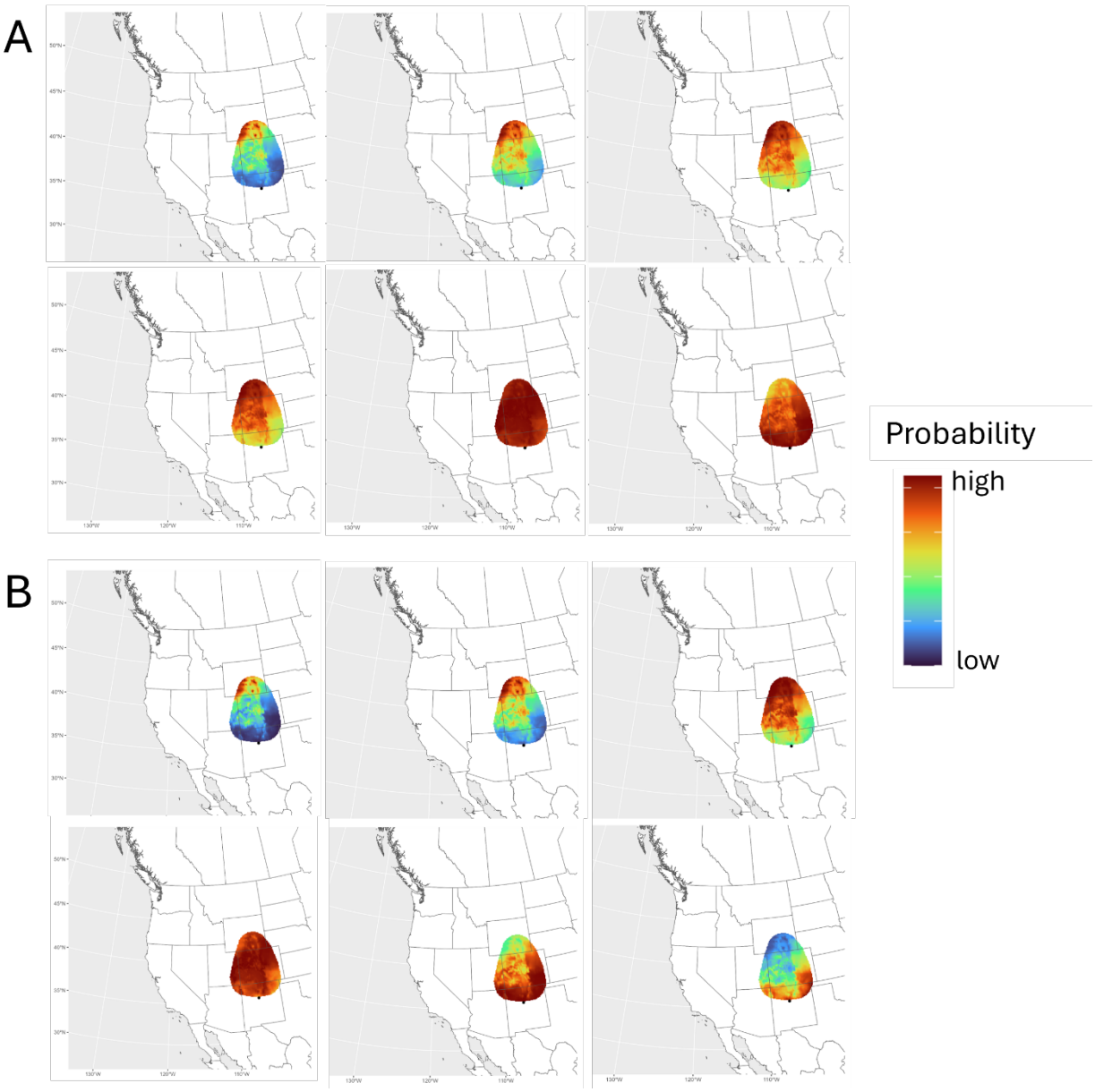

Figure 8. Probability of origin maps for BCRF juvenile (A) and adult (B) individuals based on stable hydrogen isotope values ratio (δ^2H) of feathers sampled at SACR, New Mexico 2004–2022. Values for juvenile maps have been adjusted by +10‰ to reflect the mean difference of juvenile δ^2H values from adult values. Each map represents an individual feather sample and selected maps reflect the range of probability of origin assignments generated for each age class.

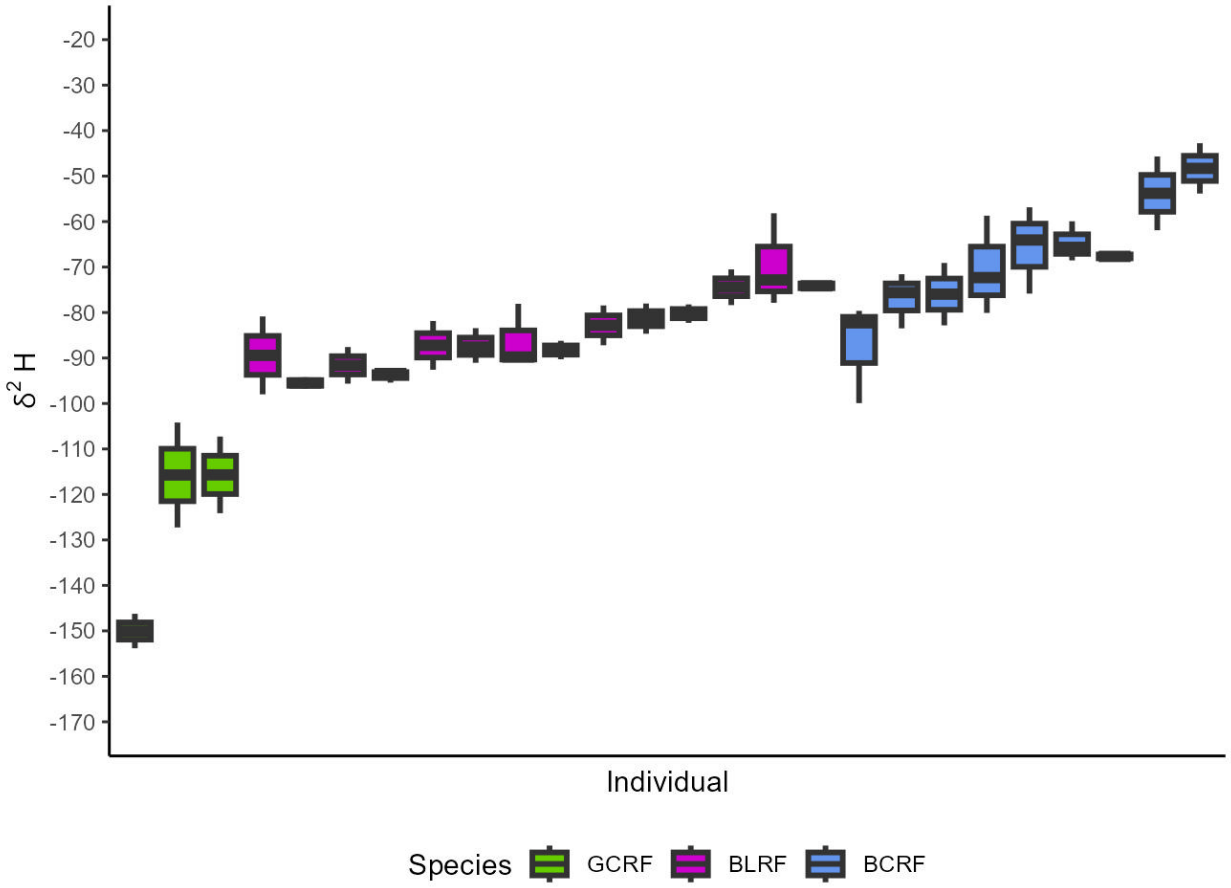

Figure 9. Stable hydrogen isotope values ratio (δ^2H) of Rosy-Finch (*Leucosticte spp.*) feathers sampled at SACR, New Mexico 2004–2022, grouped by the individual bird. Each individual shown was sampled 2–3 times as an adult during distinct winter seasons.

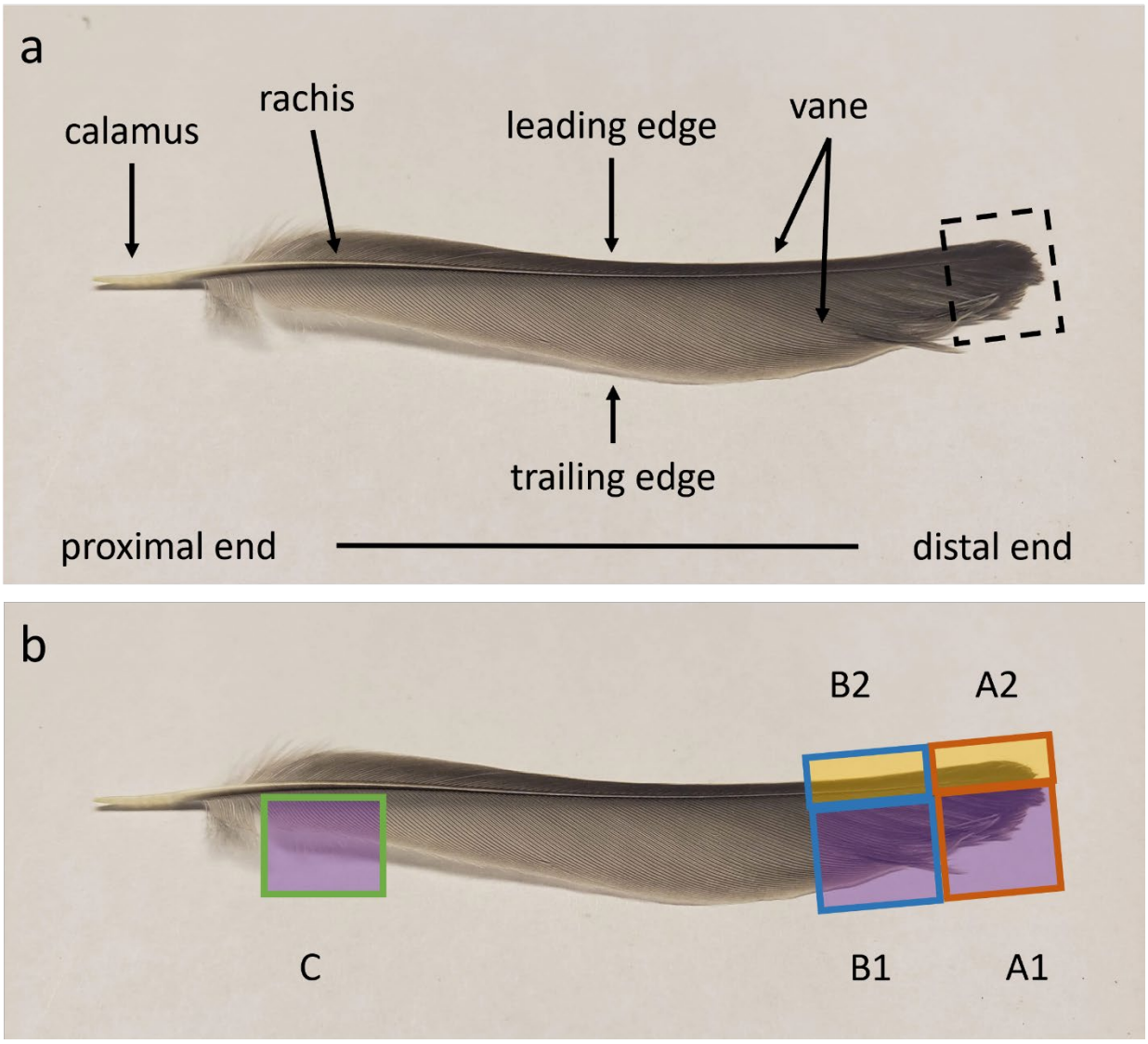

Figure 10. Feather diagrams for stable hydrogen isotope studies. Panel (a) shows general feather anatomy and sampling region for breeding origin analysis (dashed black box); panel (b) shows subsampling delineations for intra-feather variation study. Orange outlines indicate the most distal region of the feather sampled (A1 & A2); blue outlines indicate the next distal-most region (B1 & B2); green outline indicates the proximal-most feather section beyond downy barbs (C). Shapes with purple shading (A1, B2, C) distinguish feather sections excluding the rachis (i.e., the central feather shaft), from sections that include the rachis (shaded in yellow; A2 & B2).

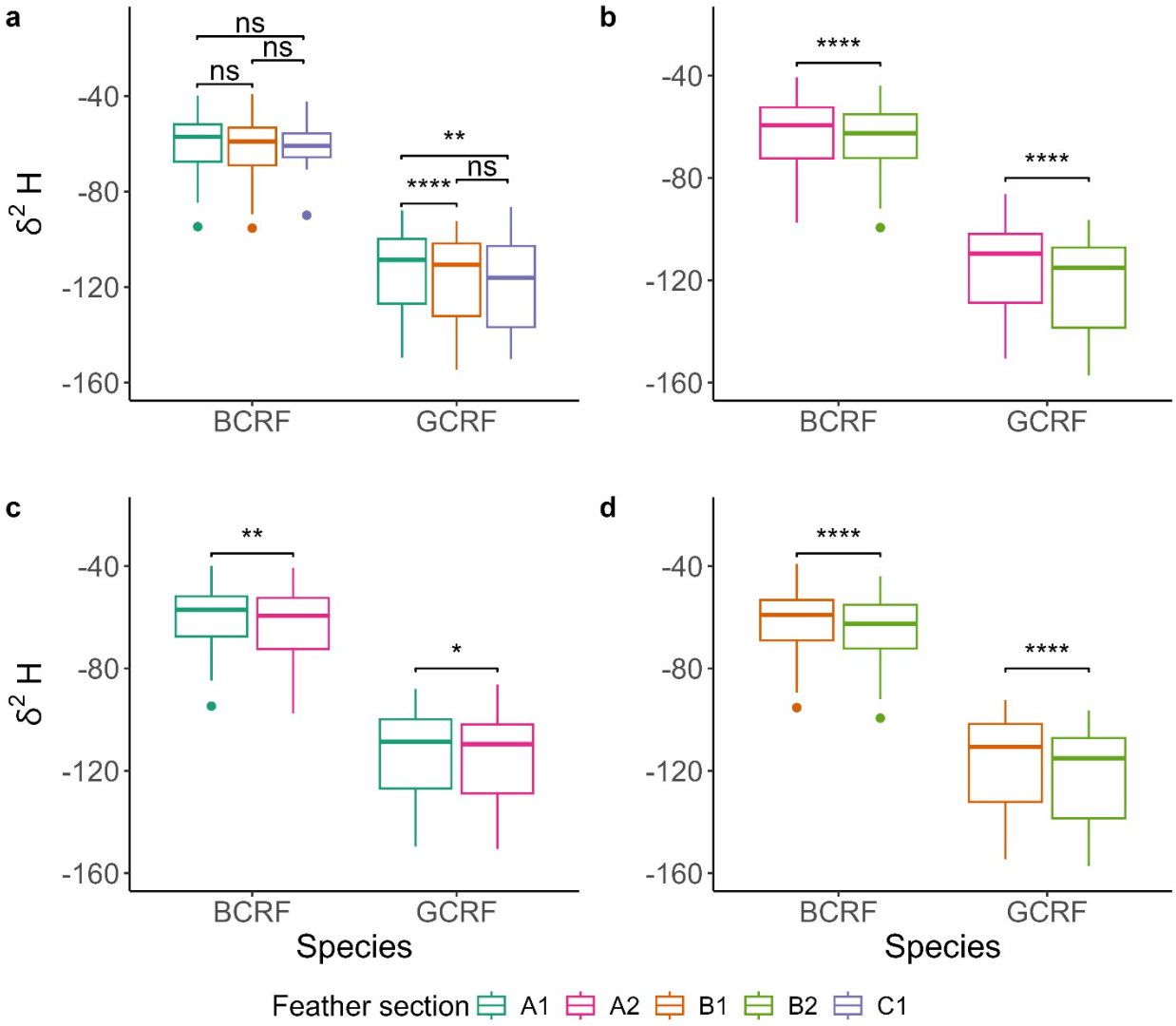

Figure 11. Boxplot and line plots for comparison of stable hydrogen isotope (δ^2H) values for different sections of BCRF and GCRF feathers collected at SACR, New Mexico 2007–2020. Feather sections are shown in Figure 10. Panels (a) and (b) compare δ^2H values of longitudinal sections; panels (c) and (d) compare values of sections containing rachis material to those containing vane material only.

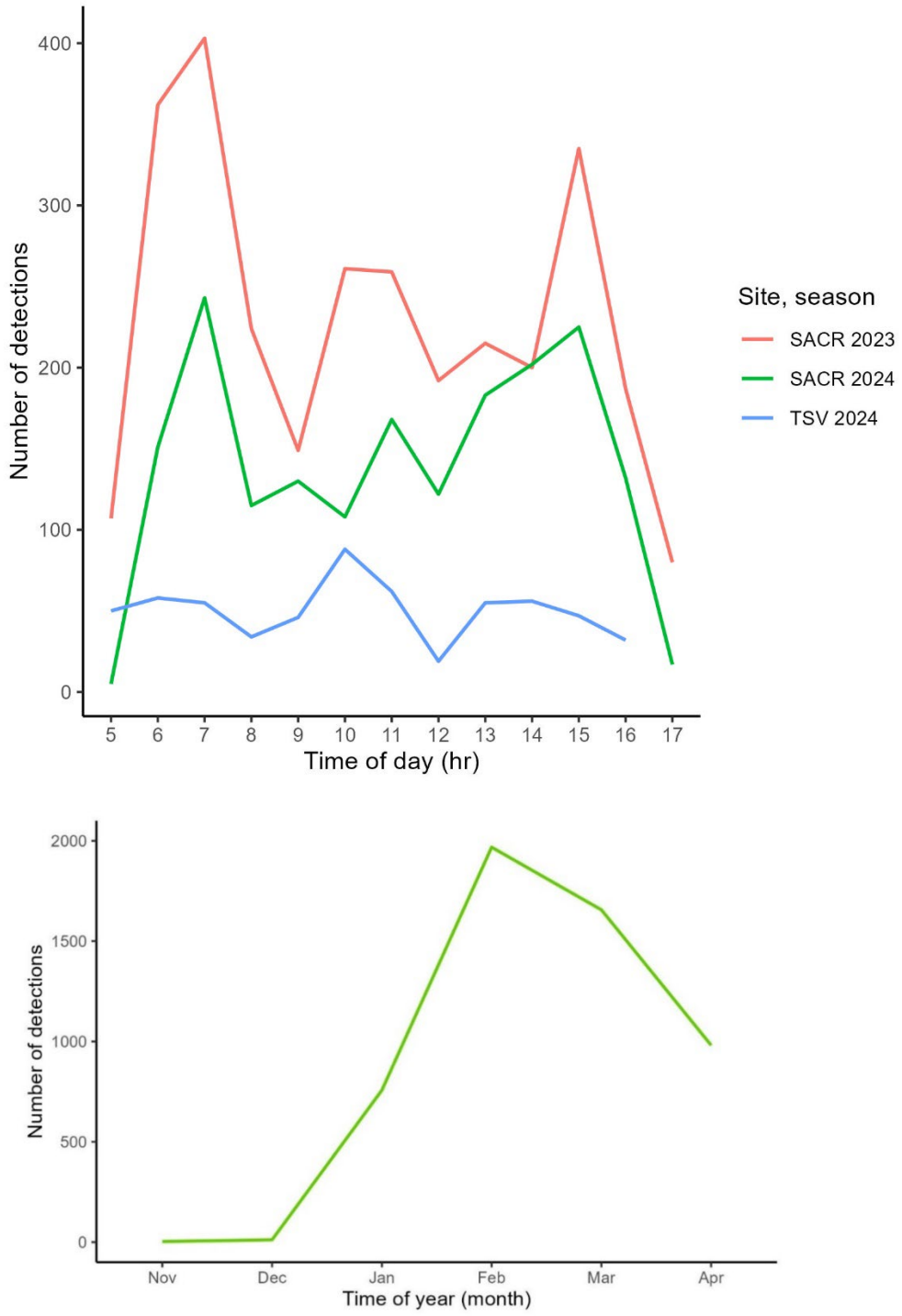

Figure 12. Temporal patterns of detections of RFID-tagged individuals by RFID-enabled feeders (top) by time of day (top) and month (bottom). In the top panel, SACR data were collected during the 2022–2023 (“2023”) and 2023–2024 (“2024”) winter seasons; TSV data were collected during the 2023–2024 (“2024”) season only. The bottom panel only includes detections from SACR because banding did not occur at TSV until April.